

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleic acid fragment which encodes at least 50 contiguous amino acids of SEQ ID NO:4, wherein said nucleic acid fragment is a fragment of a codon-optimized coding region for the polypeptide of SEQ ID NO:4;

wherein about 11 of the 24 phenylalanine codons in said coding region are TTT and about 13 of said phenylalanine codons are TTC;

wherein about 5 of the 62 leucine codons in said coding region are TTA, about 8 of said leucine codons are TTG, about 8 of said leucine codons are CTT, about 12 of said leucine codons are CTC, about 4 of said leucine codons are CTA, and about 25 of said leucine codons are CTG;

wherein about 20 of the 57 isoleucine codons in said coding region are ATT, about 28 of said isoleucine codons are ATC, and about 9 of said isoleucine codons are ATA;

wherein the 10 methionine codons in said coding region are ATG;

wherein about 8 of the 43 valine codons in said coding region are GTT, about 10 of said valine codons are GTG, about 5 of said valine codons are GTA, and about 20 of said valine codons are GTG;

wherein about 13 of the 72 serine codons in said coding region are TCT, about 16 of said serine codons are TCC, about 11 of said serine codons are TCA, about 4 of said serine codons are TCG, about 11 of said serine codons are AGT, and about 17 of said serine codons are AGC;

wherein about 8 of the 29 proline codons in said coding region are CCT, about 10 of said proline codons are CCC, about 8 of said proline codons are CCA, and about 3 of said proline codons are CCG;

wherein about 14 of the 58 threonine codons in said coding region are ACT, about 21 of said threonine codons are ACC, about 16 of said threonine codons are ACA, and about 7 of said threonine codons are ACG;

wherein about 11 of the 41 alanine codons in said coding region are GGT, about 17 of said alanine codons are GCC, about 9 of said alanine codons are GCA, and about 4 of said alanine codons are GCG;

wherein about 12 of the 28 tyrosine codons in said coding region are TAT and about 16 of said tyrosine codons are TAC;

wherein about 4 of the 10 histidine codons in said coding region are CAT and about 6 of said histidine codons are CAC;

wherein about 8 of the 31 glutamine codons in said coding region are CAA and about 23 of said glutamine codons are CAG;

wherein about 32 of the 69 asparagine codons in said coding region are AAT and about 37 of said asparagine codons are AAC;

wherein about 25 of the 60 lysine codons in said coding region are AAA and about 35 of said lysine codons are AAG;

wherein about 22 of the 47 aspartic acid codons in said coding region are GAT and about 25 of said aspartic acid codons are GAC;

wherein about 21 of the 51 glutamic acid codons in said coding region are GAA and about 30 of said glutamic acid codons are GAG;

wherein the 7 tryptophan codons in said coding region are TGG;

wherein about 2 of the 29 arginine codons in said coding region are CGT, about 6 of said arginine codons are CGC, about 3 of said arginine codons are CGA, about 6 of said arginine codons are CGG, about 6 of said arginine codons are AGA, and about 6 of said arginine codons are AGG; and

wherein about 6 of the 36 glycine codons in said coding region are GGT, about 12 of said glycine codons are GGC, about 9 of said glycine codons are GGA, and about 9 of said glycine codons are GGG.

2. The polynucleotide of claim 1, wherein said nucleic acid fragment encodes at least 100 contiguous amino acids of SEQ ID NO:4.
3. The polynucleotide of claim 2, wherein said nucleic acid fragment encodes amino acids 199 to 764 of SEQ ID NO:4.
4. The polynucleotide of claim 3, wherein said nucleic acid fragment comprises nucleotides 82 to 1782 of SEQ ID NO:1.
5. The polynucleotide of any one of claims 1-4, wherein said nucleic acid fragment is ligated to a heterologous nucleic acid.

6. The polynucleotide of claim 5, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.
7. The polynucleotide of claim 6, wherein said heterologous polypeptide is a secretory signal peptide.
8. The polynucleotide of claim 7, wherein said signal peptide is a human tissue plasminogen activator (hTPA) signal peptide.
9. The polynucleotide of claim 8, comprising nucleotides 13-1782 of SEQ ID NO:1.
10. The polynucleotide of claim 9, comprising SEQ ID NO:1.
11. The polynucleotide of claim 1, wherein said nucleic acid fragment encodes amino acids 30 to 764 of SEQ ID NO:4.
12. The polynucleotide of claim 11, wherein said nucleic acid fragment is ligated to a heterologous nucleic acid.

13. The polynucleotide of claim 12, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.

14. The polynucleotide of claim 13, wherein said heterologous polypeptide is a secretory signal peptide.

15. The polynucleotide of claim 14, wherein said signal peptide is a human tissue plasminogen activator (hTPA) signal peptide.

16. The polynucleotide of claim 11, wherein said nucleic acid fragment comprises nucleotides 88 to 2292 of SEQ ID NO:23.

17. The polynucleotide of any one of claims 1-16, which is DNA, and wherein said nucleic acid fragment is operably associated with a promoter.

18. The polynucleotide of any one of claims 1-16, which is RNA.

19. The polynucleotide of claim 18, which is messenger RNA (mRNA).

20. A vector comprising the polynucleotide of any one of claims 1-17.

21. The vector of claim 20, which is a plasmid.
22. A composition comprising the polynucleotide of any one of claims 1-19, and a carrier.
23. The composition of claim 21, further comprising a component selected from the group consisting of an adjuvant, and a transfection facilitating compound.
24. The composition of claim 23, wherein said adjuvant is selected from the group consisting of:
- (±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE) and a neutral lipid;
 - a cytokine;
 - mono-phosphoryl lipid A and trehalosedicorynomycolateAF (MPL + TDM);
 - a solubilized mono-phosphoryl lipid A formulation; and
 - CRL1005/BAK.
25. The composition of claim 24, wherein said adjuvant comprises (±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-

tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE), and wherein said neutral lipid is selected from the group consisting of:

- 1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE),
- 1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE), and
- 1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE).

26. The composition of claim 25, wherein said neutral lipid is DPyPE.

27. The composition of claim 23, comprising the transfection facilitating compound (\pm)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide (DMRIE).

28. A method to treat or prevent anthrax infection in a vertebrate comprising: administering to a vertebrate in need thereof the composition of any one of claims 22-27.

29. An isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 90% identical to amino acids 199 to 764 of SEQ ID NO:4, wherein said nucleic acid fragment is a variant fragment of an optimized coding region for the polypeptide of SEQ ID NO:4;

wherein about 11 of the 24 phenylalanine codons in said coding region are TTT and about 13 of said phenylalanine codons are TTC;

wherein about 5 of the 62 leucine codons in said coding region are TTA, about 8 of said leucine codons are TTG, about 8 of said leucine codons are CTT, about 12 of said leucine codons are CTC, about 4 of said leucine codons are CTA, and about 25 of said leucine codons are CTG;

wherein about 20 of the 57 isoleucine codons in said coding region are ATT, about 28 of said isoleucine codons are ATC, and about 9 of said isoleucine codons are ATA;

wherein the 10 methionine codons in said coding region are ATG;

wherein about 8 of the 43 valine codons in said coding region are GTT, about 10 of said valine codons are GTG, about 5 of said valine codons are GTA, and about 20 of said valine codons are GTG;

wherein about 13 of the 72 serine codons in said coding region are TCT, about 16 of said serine codons are TCC, about 11 of said serine codons are TCA, about 4 of said serine codons are TCG, about 11 of said serine codons are AGT, and about 17 of said serine codons are AGC;

wherein about 8 of the 29 proline codons in said coding region are CCT, about 10 of said proline codons are CCC, about 8 of said proline codons are CCA, and about 3 of said proline codons are CCG;

wherein about 14 of the 58 threonine codons in said coding region are ACT, about 21 of said threonine codons are ACC, about 16 of said threonine codons are ACA, and about 7 of said threonine codons are ACG;

wherein about 11 of the 41 alanine codons in said coding region are GGT, about 17 of said alanine codons are GCC, about 9 of said alanine codons are GCA, and about 4 of said alanine codons are GCG;

wherein about 12 of the 28 tyrosine codons in said coding region are TAT and about 16 of said tyrosine codons are TAC;

wherein about 4 of the 10 histidine codons in said coding region are CAT and about 6 of said histidine codons are CAC;

wherein about 8 of the 31 glutamine codons in said coding region are CAA and about 23 of said glutamine codons are CAG;

wherein about 32 of the 69 asparagine codons in said coding region are AAT and about 37 of said asparagine codons are AAC;

wherein about 25 of the 60 lysine codons in said coding region are AAA and about 35 of said lysine codons are AAG;

wherein about 22 of the 47 aspartic acid codons in said coding region are GAT and about 25 of said aspartic acid codons are GAC;

wherein about 21 of the 51 glutamic acid codons in said coding region are GAA and about 30 of said glutamic acid codons are GAG;

wherein the 7 tryptophan codons in said coding region are TGG;

wherein about 2 of the 29 arginine codons in said coding region are CGT, about 6 of said arginine codons are CGC, about 3 of said arginine codons are CGA, about 6 of said arginine codons are CGG, about 6 of said arginine codons are AGA, and about 6 of said arginine codons are AGG; and

wherein about 6 of the 36 glycine codons in said coding region are GGT, about 12 of said glycine codons are GGC, about 9 of said glycine codons are GGA, and about 9 of said glycine codons are GGG.

30. The polynucleotide of claim 29, wherein said nucleic acid fragment encodes a polypeptide at least 95% identical to amino acids 199 to 764 of SEQ ID NO:4.

31. The polynucleotide of claim 29, wherein the codons in said nucleic acid fragment corresponding to amino acids 342 and 343 of SEQ ID NO:4 are deleted.

32. The polynucleotide of claim 31, wherein said nucleic acid fragment encodes amino acids 24 to 587 of SEQ ID NO:6.

33. The polynucleotide of claim 32, which comprises nucleotides 82 to 1773 of SEQ ID NO:5.

34. The polynucleotide of claim 29, wherein the asparagine codons in said nucleic acid fragment corresponding to amino acids 275, 321, 357, 417, 505, 538, 599, 650, 693, and 738 of SEQ ID NO:4 are deleted and each of said asparagine codons is replaced with a codon which codes for an amino acid other than asparagine.

35. The polynucleotide of claim 34, wherein the asparagine codons in said nucleic acid fragment corresponding to amino acids 275, 321, 357, 417, 505, 538, 599, 650, 693, and 738 of SEQ ID NO:4 are deleted and each of said asparagine codons replaced with a codon which codes for glutamine.

36. The polynucleotide of claim 35, wherein said nucleic acid fragment encodes amino acids 24 to 589 of SEQ ID NO:18.

37. The polynucleotide of claim 36, which comprises nucleotides 82 to 1779 of SEQ ID NO:17.

38. The polynucleotide of claim 31, wherein the asparagine codons in said nucleic acid fragment corresponding to amino acids 275, 321, 357, 417, 505, 538, 599, 650, 693, and 738 of SEQ ID NO:4 are deleted and each of said asparagine codons is replaced with a codon which codes for an amino acid other than asparagine.

39. The polynucleotide of claim 38, wherein the asparagine codons in said nucleic acid fragment corresponding to amino acids 39, 153, 275, 321, 357, 417, 505, 538, 599, 650, 693, and 738 of SEQ ID NO:4 are deleted and each of said asparagine codons replaced with a codon which codes for glutamine.

40. The polynucleotide of any one of claims 29-39, wherein said nucleic acid fragment is ligated to a heterologous nucleic acid.

41. The polynucleotide of claim 40, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.

42. The polynucleotide of claim 41, wherein said heterologous polypeptide is a secretory signal peptide.

43. The polynucleotide of claim 42, wherein said signal peptide is a human tissue plasminogen activator (hTPA) signal peptide.

44. The polynucleotide of any one of claims 29-43, which is DNA, and wherein said nucleic acid fragment is operably associated with a promoter.

45. The polynucleotide of any one of claims 29-43, which is RNA.

46. The polynucleotide of claim 45, which is messenger RNA (mRNA).

47. A vector comprising the polynucleotide of any one of claims 29-44.

48. The vector of claim 47, which is a plasmid.

49. A composition comprising the polynucleotide of any one of claims 29-46, and a carrier.

50. The composition of claim 49, further comprising a component selected from the group consisting of an adjuvant, and a transfection facilitating compound.

51. The composition of claim 50, wherein said adjuvant is selected from the group consisting of:

(±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE) and a neutral lipid;

a cytokine;

mono-phosphoryl lipid A and trehalosedicorynomycolateAF (MPL + TDM);

a solubilized mono-phosphoryl lipid A formulation; and

CRL1005/BAK.

52. The composition of claim 51, wherein said adjuvant comprises(\pm)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE), and wherein said neutral lipid is selected from the group consisting of:

1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE),
1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE), and
1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE).

53. The composition of claim 52, wherein said neutral lipid is DPyPE.

54. The composition of claim 50, comprising the transfection facilitating compound (\pm)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide) (DMRIE).

55. A method to treat or prevent anthrax infection in a vertebrate comprising: administering to a vertebrate in need thereof the composition of any one of claims 49-54.

56. An isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 90% identical to amino acids 30 to 764 of SEQ ID NO:4, wherein said nucleic acid fragment is a variant fragment of an optimized coding region for the polypeptide of SEQ ID NO:4;

wherein about 11 of the 24 phenylalanine codons in said coding region are TTT and about 13 of said phenylalanine codons are TTC;

wherein about 5 of the 62 leucine codons in said coding region are TTA, about 8 of said leucine codons are TTG, about 8 of said leucine codons are CTT, about 12 of said leucine codons are CTC, about 4 of said leucine codons are CTA, and about 25 of said leucine codons are CTG;

wherein about 20 of the 57 isoleucine codons in said coding region are ATT, about 28 of said isoleucine codons are ATC, and about 9 of said isoleucine codons are ATA;

wherein the 10 methionine codons in said coding region are ATG;

wherein about 8 of the 43 valine codons in said coding region are GTT, about 10 of said valine codons are GTG, about 5 of said valine codons are GTA, and about 20 of said valine codons are GTG;

wherein about 13 of the 72 serine codons in said coding region are TCT, about 16 of said serine codons are TCC, about 11 of said serine codons are TCA, about 4 of said serine codons are TCG, about 11 of said serine codons are AGT, and about 17 of said serine codons are AGC;

wherein about 8 of the 29 proline codons in said coding region are CCT, about 10 of said proline codons are CCC, about 8 of said proline codons are CCA, and about 3 of said proline codons are CCG;

wherein about 14 of the 58 threonine codons in said coding region are ACT, about 21 of said threonine codons are ACC, about 16 of said threonine codons are ACA, and about 7 of said threonine codons are ACG;

wherein about 11 of the 41 alanine codons in said coding region are GGT, about 17 of said alanine codons are GCC, about 9 of said alanine codons are GCA, and about 4 of said alanine codons are GCG;

wherein about 12 of the 28 tyrosine codons in said coding region are TAT and about 16 of said tyrosine codons are TAC;

wherein about 4 of the 10 histidine codons in said coding region are CAT and about 6 of said histidine codons are CAC;

wherein about 8 of the 31 glutamine codons in said coding region are CAA and about 23 of said glutamine codons are CAG;

wherein about 32 of the 69 asparagine codons in said coding region are AAT and about 37 of said asparagine codons are AAC;

wherein about 25 of the 60 lysine codons in said coding region are AAA and about 35 of said lysine codons are AAG;

wherein about 22 of the 47 aspartic acid codons in said coding region are GAT and about 25 of said aspartic acid codons are GAC;

wherein about 21 of the 51 glutamic acid codons in said coding region are GAA and about 30 of said glutamic acid codons are GAG;

wherein the 7 tryptophan codons in said coding region are TGG;

wherein about 2 of the 29 arginine codons in said coding region are CGT, about 6 of said arginine codons are CGC, about 3 of said arginine codons are CGA, about 6 of said arginine codons are CGG, about 6 of said arginine codons are AGA, and about 6 of said arginine codons are AGG; and

wherein about 6 of the 36 glycine codons in said coding region are GGT, about 12 of said glycine codons are GGC, about 9 of said glycine codons are GGA, and about 9 of said glycine codons are GGG.

57. The polynucleotide of claim 56, wherein said nucleic acid fragment encodes a polypeptide at least 95% identical to amino acids 30 to 764 of SEQ ID NO:4.

58. The polynucleotide of claim 56, wherein the codons in said nucleic acid fragment corresponding to amino acids 192 to 197 of SEQ ID NO:4 are deleted.

59. The polynucleotide of claim 58, wherein said nucleic acid fragment encodes amino acids 24 to 752 of SEQ ID NO:8.

60. The polynucleotide of claim 59, which comprises nucleotides 82 to 2268 of SEQ ID NO:7.

61. The polynucleotide of claim 56, wherein the asparagine codons in said nucleic acid fragment corresponding to amino acids 39, 153, 275, 321, 357, 417, 505, 538, 599, 650, 693, and 738 of SEQ ID NO:4 are deleted and each of said asparagine codons is replaced with a codon which codes for an amino acid other than asparagine.

62. The polynucleotide of claim 61, wherein the asparagine codons in said nucleic acid fragment corresponding to amino acids 39, 153, 275, 321, 357, 417, 505, 538, 599, 650, 693, and 738 of SEQ ID NO:4 are deleted and each of said asparagine codons replaced with a codon which codes for glutamine.

63. The polynucleotide of claim 58, wherein the asparagine codons in said nucleic acid fragment corresponding to amino acids 39, 153, 275, 321, 357, 417, 505, 538, 599, 650, 693, and 738 of SEQ ID NO:4 are deleted and each of said asparagine codons is replaced with a codon which codes for an amino acid other than asparagine.

64. The polynucleotide of claim 63, wherein the asparagine codons in said nucleic acid fragment corresponding to amino acids 39, 153, 275, 321, 357, 417, 505, 538, 599, 650, 693, and 738 of SEQ ID NO:AP are deleted and each of said asparagine codons replaced with a codon which codes for glutamine.

65. The polynucleotide of any one of claims 56-64, wherein said nucleic acid fragment is ligated to a heterologous nucleic acid.

66. The polynucleotide of claim 65, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.

67. The polynucleotide of claim 66, wherein said heterologous polypeptide is a secretory signal peptide.

68. The polynucleotide of claim 67, wherein said signal peptide is a human tissue plasminogen activator (hTPA) signal peptide.

69. The polynucleotide of any one of claims 56-68, which is DNA, and wherein said nucleic acid fragment is operably associated with a promoter.

70. The polynucleotide of any one of claims 56-68, which is RNA.

71. The polynucleotide of claim 70, which is messenger RNA (mRNA).

72. A vector comprising the polynucleotide of any one of claims 56-69.

73. The vector of claim 72, which is a plasmid.

74. A composition comprising the polynucleotide of any one of claims 56-71, and a carrier.

75. The composition of claim 74, further comprising a component selected from the group consisting of an adjuvant, and a transfection facilitating compound.

76. The composition of claim 75, wherein said adjuvant is selected from the group consisting of:

(±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE) and a neutral lipid;
a cytokine;
mono-phosphoryl lipid A and trehalosedicorynomycolateAF (MPL + TDM);
a solubilized mono-phosphoryl lipid A formulation; and
CRL1005/BAK.

77. The composition of claim 76, wherein said adjuvant comprises (±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE), and wherein said neutral lipid is selected from the group consisting of:

1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE),
1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE), and

1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE).

78. The composition of claim 77, wherein said neutral lipid is DPyPE.

79. The composition of claim 75, comprising the transfection facilitating compound (\pm)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide) (DMRIE).

80. A method to treat or prevent anthrax infection in a vertebrate comprising: administering to a vertebrate in need thereof the composition of any one of claims 74-79.

81. An isolated polynucleotide comprising a nucleic acid fragment which encodes at least 50 contiguous amino acids of SEQ ID NO:12, wherein said nucleic acid fragment is a portion of an optimized coding region for the polypeptide of SEQ ID NO:12;

wherein about 13 of the 29 phenylalanine codons in said coding region are TTT and about 16 of said phenylalanine codons are TTC;

wherein about 6 of the 80 leucine codons in said coding region are TTA, about 10 of said leucine codons are TTG, about 10 of said leucine codons are CTT, about 16 of said leucine codons are CTC, about 6 of said leucine codons are CTA, and about 32 of said leucine codons are CTG;

wherein about 26 of the 74 isoleucine codons in said coding region are ATT, about 36 of said isoleucine codons are ATC, and about 12 of said isoleucine codons are ATA;

wherein the 10 methionine codons in said coding region are ATG;

wherein about 7 of the 40 valine codons in said coding region are GTT, about 9 of said valine codons are GTG, about 5 of said valine codons are GTA, and about 19 of said valine codons are GTG;

wherein about 10 of the 54 serine codons in said coding region are TCT, about 12 of said serine codons are TCC, about 8 of said serine codons are TCA, about 3 of said serine codons are TCG, about 8 of said serine codons are AGT, and about 13 of said serine codons are AGC;

wherein about 6 of the 21 proline codons in said coding region are CCT, about 7 of said proline codons are CCC, about 6 of said proline codons are CCA, and about 2 of said proline codons are CCG;

wherein about 7 of the 28 threonine codons in said coding region are ACT, about 10 of said threonine codons are ACC, about 8 of said threonine codons are ACA, and about 3 of said threonine codons are ACG;

wherein about 9 of the 34 alanine codons in said coding region are GGT, about 14 of said alanine codons are GCC, about 8 of said alanine codons are GCA, and about 3 of said alanine codons are GCG;

wherein about 15 of the 35 tyrosine codons in said coding region are TAT and about 20 of said tyrosine codons are TAC;

wherein about 9 of the 21 histidine codons in said coding region are CAT and about 12 of said histidine codons are CAC;

wherein about 10 of the 41 glutamine codons in said coding region are CAA and about 31 of said glutamine codons are CAG;

wherein about 25 of the 54 asparagine codons in said coding region are AAT and about 29 of said asparagine codons are AAC;

wherein about 36 of the 86 lysine codons in said coding region are AAA and about 50 of said lysine codons are AAG;

wherein about 25 of the 55 aspartic acid codons in said coding region are GAT and about 30 of said aspartic acid codons are GAC;

wherein about 33 of the 79 glutamic acid codons in said coding region are GAA and about 46 of said glutamic acid codons are GAG;

wherein the single cysteine codon in said coding region is selected from the group consisting of TGT and TGC;

wherein the 5 tryptophan codons in said coding region are TGG;

wherein about 2 of the 27 arginine codons in said coding region are CGT, about 5 of said arginine codons are CGC, about 3 of said arginine codons are CGA, about 6 of said arginine codons are CGG, about 6 of said arginine codons are AGA, and about 5 of said arginine codons are AGG; and

wherein about 6 of the 35 glycine codons in said coding region are GGT, about 12 of said glycine codons are GGC, about 8 of said glycine codons are GGA, and about 9 of said glycine codons are GGG.

82. The polynucleotide of claim 81, wherein said cysteine codon in said coding region is TGT.

83. The polynucleotide of claim 81, wherein said cysteine codon in said coding region is TGC.

84. The polynucleotide of claim 81, wherein said nucleic acid fragment encodes at least 100 contiguous amino acids of SEQ ID NO:12.

85. The polynucleotide of claim 84, wherein said nucleic acid fragment encodes amino acids 34 to 809 of SEQ ID NO:12.

86. The polynucleotide of claim 85, wherein said nucleic acid fragment comprises nucleotides 99 to 2427 of SEQ ID NO:26.

87. The polynucleotide of claim 81, wherein said nucleic acid fragment encodes amino acids 34-583 of SEQ ID NO:12.

88. The polynucleotide of claim 81, wherein said nucleic acid fragment encodes amino acids 34-254 of SEQ ID NO:12.

89. The polynucleotide of claim 81, wherein said nucleic acid fragment encodes amino acids 34-295 of SEQ ID NO:12.

90. The polynucleotide of any one of claims 81-89, wherein said nucleic acid fragment is ligated to a heterologous nucleic acid.

91. The polynucleotide of claim 90, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.

92. The polynucleotide of claim 91, wherein said heterologous polypeptide is a secretory signal peptide.

93. The polynucleotide of claim 92, wherein said signal peptide is a human tissue plasminogen activator (hTPA) signal peptide.

94. The polynucleotide of any one of claims 81-93, which is DNA, and wherein said nucleic acid fragment is operably associated with a promoter.

95. The polynucleotide of any one of claims 81-93, which is RNA.

96. The polynucleotide of claim 95, which is messenger RNA (mRNA).

97. A vector comprising the polynucleotide of any one of claims 81-94.

98. The vector of claim 97, which is a plasmid.

99. A composition comprising the polynucleotide of any one of claims 81-96, and a carrier.

100. The composition of claim 99, further comprising a component selected from the group consisting of an adjuvant, and a transfection facilitating compound.

101. The composition of claim 100, wherein said adjuvant is selected from the group consisting of:

(±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE) and a neutral lipid;

a cytokine;

mono-phosphoryl lipid A and trehalosedicorynomycolateAF (MPL + TDM);

a solubilized mono-phosphoryl lipid A formulation; and

CRL1005/BAK.

102. The composition of claim 101, wherein said adjuvant comprises(\pm)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE), and wherein said neutral lipid is selected from the group consisting of:

1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE),
1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE), and
1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE).

103. The composition of claim 102, wherein said neutral lipid is DPyPE.

104. The composition of claim 100, comprising the transfection facilitating compound (\pm)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide) (DMRIE).

105. A method to treat or prevent anthrax infection in a vertebrate comprising: administering to a vertebrate in need thereof the composition of any one of claims 99-104.

106. An isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 90% identical to amino acids 34 to 809 of SEQ ID NO:12, wherein said nucleic acid fragment is a variant fragment of an optimized coding region for the polypeptide of SEQ ID NO:12;

wherein about 13 of the 29 phenylalanine codons in said coding region are TTT and about 16 of said phenylalanine codons are TTC;

wherein about 6 of the 80 leucine codons in said coding region are TTA, about 10 of said leucine codons are TTG, about 10 of said leucine codons are CTT, about 16 of said leucine codons are CTC, about 6 of said leucine codons are CTA, and about 32 of said leucine codons are CTG;

wherein about 26 of the 74 isoleucine codons in said coding region are ATT, about 36 of said isoleucine codons are ATC, and about 12 of said isoleucine codons are ATA;

wherein the 10 methionine codons in said coding region are ATG;

wherein about 7 of the 40 valine codons in said coding region are GTT, about 9 of said valine codons are GTG, about 5 of said valine codons are GTA, and about 19 of said valine codons are GTG;

wherein about 10 of the 54 serine codons in said coding region are TCT, about 12 of said serine codons are TCC, about 8 of said serine codons are TCA, about 3 of said serine codons are TCG, about 8 of said serine codons are AGT, and about 13 of said serine codons are AGC;

wherein about 6 of the 21 proline codons in said coding region are CCT, about 7 of said proline codons are CCC, about 6 of said proline codons are CCA, and about 2 of said proline codons are CCG;

wherein about 7 of the 28 threonine codons in said coding region are ACT, about 10 of said threonine codons are ACC, about 8 of said threonine codons are ACA, and about 3 of said threonine codons are ACG;

wherein about 9 of the 34 alanine codons in said coding region are GGT, about 14 of said alanine codons are GCC, about 8 of said alanine codons are GCA, and about 3 of said alanine codons are GCG;

wherein about 15 of the 35 tyrosine codons in said coding region are TAT and about 20 of said tyrosine codons are TAC;

wherein about 9 of the 21 histidine codons in said coding region are CAT and about 12 of said histidine codons are CAC;

wherein about 10 of the 41 glutamine codons in said coding region are CAA and about 31 of said glutamine codons are CAG;

wherein about 25 of the 54 asparagine codons in said coding region are AAT and about 29 of said asparagine codons are AAC;

wherein about 36 of the 86 lysine codons in said coding region are AAA and about 50 of said lysine codons are AAG;

wherein about 25 of the 55 aspartic acid codons in said coding region are GAT and about 30 of said aspartic acid codons are GAC;

wherein about 33 of the 79 glutamic acid codons in said coding region are GAA and about 46 of said glutamic acid codons are GAG;

wherein the single cysteine codon in said coding region is selected from the group consisting of TGT and TGC;

wherein the 5 tryptophan codons in said coding region are TGG;

wherein about 2 of the 27 arginine codons in said coding region are CGT, about 5 of said arginine codons are CGC, about 3 of said arginine

codons are CGA, about 6 of said arginine codons are CGG, about 6 of said arginine codons are AGA, and about 5 of said arginine codons are AGG; and wherein about 6 of the 35 glycine codons in said coding region are GGT, about 12 of said glycine codons are GGC, about 8 of said glycine codons are GGA, and about 9 of said glycine codons are GGG.

107. The polynucleotide of claim 106, wherein said cysteine codon in said coding region is TGT.

108. The polynucleotide of claim 106, wherein said cysteine codon in said coding region is TGC.

109. The polynucleotide of claim 106, wherein nucleic acid fragment encodes a polypeptide at least 95% identical to amino acids 34 to 809 of SEQ ID NO:12.

110. The polynucleotide of claim 106, wherein the histidine codons in said nucleic acid fragment corresponding to positions 719 and 723 of SEQ ID NO:12 are deleted and each is replaced with a codon which codes for an amino acid other than histidine, and wherein the glutamic acid codon in said nucleic acid fragment corresponding to position 720 of SEQ ID NO:12 is deleted and replaced with a codon which codes for an amino acid other than glutamic acid.

111. The polynucleotide of claim 110, wherein the histidine codons in said nucleic acid fragment corresponding to positions 719 and 723 of SEQ ID NO:12 are deleted and each is replaced with an alanine codon selected from the group consisting of GCT, GCC, GCA, and GCG, and wherein the glutamic acid codon in said nucleic acid fragment corresponding to position 720 of SEQ ID NO:12 is deleted and replaced with an aspartic acid codon selected from the group consisting of GAT and GAC.

112. The polynucleotide of claim 111, which comprises nucleotides 82 to 2409 of SEQ ID NO:9.

113. The polynucleotide of claim 106, wherein the asparagine codons in said nucleic acid fragment corresponding to positions 62, 212, 286, 478, 712, 736, and 757 of SEQ ID NO:12 are deleted and each is replaced with a codon which codes for an amino acid other than asparagine.

114. The polynucleotide of claim 113, wherein the asparagine codons in said nucleic acid fragment corresponding to positions 62, 212, 286, 478, 712, 736, and 757 of SEQ ID NO:12 are deleted and each is replaced with a glutamine codon selected from the group consisting of CAA and CAG.

115. The polynucleotide of claim 110, wherein the asparagine codons in said nucleic acid fragment corresponding to positions 62, 212, 286, 478, 712, 736, and 757 of SEQ ID NO:12 are deleted and each is replaced with a codon which codes for an amino acid other than asparagine.

116. The polynucleotide of claim 115, wherein the asparagine codons in said nucleic acid fragment corresponding to positions 62, 212, 286, 478, 712, 736, and 757 of SEQ ID NO:12 are deleted and each is replaced with a glutamine codon selected from the group consisting of CAA and CAG.

117. The polynucleotide of claim 116, wherein said glutamine codon is CAA.

118. The polynucleotide of claim 116, wherein said glutamine codon is CAG.

119. The polynucleotide of claim 116, which comprises nucleotides 82 to 2409 of SEQ ID NO:19.

120. The polynucleotide of any one of claims 106-119, wherein said nucleic acid fragment is ligated to a heterologous nucleic acid.

121. The polynucleotide of claim 120, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.

122. The polynucleotide of claim 121, wherein said heterologous polypeptide is a secretory signal peptide.

123. The polynucleotide of claim 122, wherein said signal peptide is a human tissue plasminogen activator (hTPA) signal peptide.

124. The polynucleotide of any one of claims 106-123, which is DNA, and wherein said nucleic acid fragment is operably associated with a promoter.

125. The polynucleotide of any one of claims 106-123, which is RNA.

126. The polynucleotide of claim 125, which is messenger RNA (mRNA).

127. A vector comprising the polynucleotide of any one of claims 106-124.

128. The vector of claim 127, which is a plasmid.

129. A composition comprising the polynucleotide of any one of claims 106-126, and a carrier.

130. The composition of claim 129, further comprising a component selected from the group consisting of an adjuvant, and a transfection facilitating compound.

131. The composition of claim 130, wherein said adjuvant is selected from the group consisting of:

(±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE) and a neutral lipid;

a cytokine;

mono-phosphoryl lipid A and trehalosedicorynomycolateAF (MPL + TDM);

a solubilized mono-phosphoryl lipid A formulation; and

CRL1005/BAK.

132. The composition of claim 131, wherein said adjuvant comprises(±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE), and wherein said neutral lipid is selected from the group consisting of:

1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE),
1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE), and
1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE).

133. The composition of claim 132, wherein said neutral lipid is DPyPE.

134. The composition of claim 130, comprising the transfection facilitating compound (\pm)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide) (DMRIE).

135. A method to treat or prevent anthrax infection in a vertebrate comprising: administering to a vertebrate in need thereof the composition of any one of claims 129-134.